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The chemical base for white tea quality: Oligopeptide, nuculeotides, and beyond

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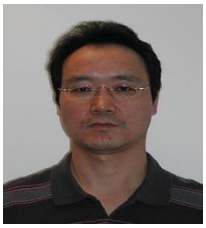

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Abstract

Among the six types of chinese tea (green tea, white tea, yellow tea, Oolong tea, black tea, and dark tea), white tea mainly is produced in southeast part of China from several selected tea cultivars. The manufacture of white is the simplest one, constitued by only two steps, they are : prolonged withering and fixation. The white tea is characterized by "umami" taste, and becomes incresingly popular in both international and domestic markets. Previous studies suggested that the relative high contents of free amion acids from white tea attribute to its characteristic taste. Here, we investigated whether other chemicals could potentially contribute to its unique flavour, such as oligopeptides and nucleotides. We also explored the chemical differences among different grades of white tea. Our studies provide new insights about the chemicals to shape white tea flavour.

Biography:

Mingjie Chen has completed his PhD from Shanghai Institute of Plant Physiology and Ecology and postdoctoral studies from University of Minnesota and University of Missouri. He is the distinguished professor of Xinyang Normal University. He has published more than 25 papers in reputed journals. His current reserach interests focus on understanding the chemical base of tea quality, tea lipid metabolism, and new method developments for tea research.

Speaker Publications:

1. "Characterization of low temperature-induced plasma membrane lipidome remodeling combined with gene expression analysis reveals mechanisms that regulate membrane lipid desaturation in Carica papaya"; Scientia Horticulturae/2020/ https://doi.org/10.1016/j.scienta.2020.109505
2. "A Proposed Method for Simultaneous Measurement of Cuticular Transpiration from Different Leaf Surfaces in Camellia sinensis"; Frontier in Plant Sciences/2020/ doi: 10.3389/fpls.2020.00420
3. "Location affects fatty acid composition in Camellia sinensis cv Tieguanyin fresh leaves"; Journal of Food Science and Technology/2019/57(1)/pp 96-101. doi: 10.1007/s13197-019-04034-8.
4. "Establishing a System for Functional Characterization of Full-Length cDNAs of Camellia sinensis"; International Journal of Molecular Science/2019/20/5929; doi:10.3390/ijms20235929
5. "Volatile component quantification in combination with putative gene expression analysis reveal key players in aroma formation during fruit ripening in Carica papaya cv Hong fei"; Postharvest Biology and Technology/2019/158/110987

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